

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 09/696,709  
Source: IFW16  
Date Processed by STIC: 11-10-2004

# ***ENTERED***



IFW16

RAW SEQUENCE LISTING                      DATE: 11/10/2004  
 PATENT APPLICATION: US/09/696,709              TIME: 10:22:27

Input Set : N:\CrF3\RULE60\09696709.raw.txt  
 Output Set: N:\CRF4\11102004\I696709.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:  
 5     (i) APPLICANT: Lambert, Lewis H., Jr.  
 7     (ii) TITLE OF INVENTION: Improved Therapeutic Compositions Comprising  
 8                                      Bactericidal/Permeability-Increasing (BPI) Protein  
 Products  
 10     (iii) NUMBER OF SEQUENCES: 2  
 12     (iv) CORRESPONDENCE ADDRESS:  
 13         (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 14         (B) STREET: 6300 Sears Tower, 233 South Wacker Drive  
 15         (C) CITY: Chicago  
 16         (D) STATE: Illinois  
 17         (E) COUNTRY: United States of America  
 18         (F) ZIP: 60606-6402  
 20     (v) COMPUTER READABLE FORM:  
 21         (A) MEDIUM TYPE: Floppy disk  
 22         (B) COMPUTER: IBM PC compatible  
 23         (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 24         (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
 26     (vi) CURRENT APPLICATION DATA:  
 C--> 27         (A) APPLICATION NUMBER: US/09/696,709  
 C--> 28         (B) FILING DATE: 24-Oct-2000  
 W--> 36         (C) CLASSIFICATION: 514  
 31     (vii) PRIOR APPLICATION DATA:  
 W--> 32         (A) APPLICATION NUMBER: US/08/586,133  
 33         (B) FILING DATE: 12-JAN-1996  
 W--> 34         (A) APPLICATION NUMBER: US 08/372,104  
 35         (B) FILING DATE: 13-JAN-1995  
 38     (viii) ATTORNEY/AGENT INFORMATION:  
 39         (A) NAME: Sharp, Jeffrey S.  
 40         (B) REGISTRATION NUMBER: 31,879  
 41         (C) REFERENCE/DOCKET NUMBER: 27129/33071  
 43     (ix) TELECOMMUNICATION INFORMATION:  
 44         (A) TELEPHONE: 312/474-6300  
 45         (B) TELEFAX: 312/474-0448  
 46         (C) TELEX: 25-3856  
 49 (2) INFORMATION FOR SEQ ID NO: 1:  
 51     (i) SEQUENCE CHARACTERISTICS:  
 52         (A) LENGTH: 1813 base pairs  
 53         (B) TYPE: nucleic acid  
 54         (C) STRANDEDNESS: single  
 55         (D) TOPOLOGY: linear  
 57     (ii) MOLECULE TYPE: cDNA  
 60     (ix) FEATURE:

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61      (A) NAME/KEY: CDS
62      (B) LOCATION: 31..1491
64      (ix) FEATURE:
65          (A) NAME/KEY: mat_peptide
66          (B) LOCATION: 124..1491
68      (ix) FEATURE:
69          (A) NAME/KEY: misc_feature
71          (D) OTHER INFORMATION: "rBPI"
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76 CAGGCCTTGA GGTTTTGGCA GCTCTGGAGG ATG AGA GAG AAC ATG GCC AGG GGC      54
77                               Met Arg Glu Asn Met Ala Arg Gly
78                               -31 -30                               -25
80 CCT TGC AAC GCG CCG AGA TGG GTG TCC CTG ATG GTG CTC GTC GCC ATA      102
81 Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
82                               -20                               -15                               -10
84 GGC ACC GCC GTG ACA GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC      150
85 Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
86                               -5                               1                               5
88 TCC CAG AAG GGC CTG GAC TAC GCC AGC CAG CAG GGG ACG GCC GCT CTG      198
89 Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
90 10                               15                               20                               25
92 CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC TAC TCA GAC AGC TTT      246
93 Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe
94                               30                               35                               40
96 AAG ATC AAG CAT CTT GGG AAG GGG CAT TAT AGC TTC TAC AGC ATG GAC      294
97 Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp
98                               45                               50                               55
100 ATC CGT GAA TTC CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT      342
101 Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn
102                               60                               65                               70
104 GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG ATC AGC GGG      390
105 Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly
106                               75                               80                               85
108 AAA TGG AAG GCA CAA AAG AGA TTC TTA AAA ATG AGC GGC AAT TTT GAC      438
109 Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp
110 90                               95                               100                               105
112 CTG AGC ATA GAA GGC ATG TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT      486
113 Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser
114                               110                               115                               120
116 AAC CCC ACG TCA GGC AAG CCC ACC ATC ACC TGC TCC AGC TGC AGC AGC      534
117 Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser
118                               125                               130                               135
120 CAC ATC AAC AGT GTC CAC GTG CAC ATC TCA AAG AGC AAA GTC GGG TGG      582
121 His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp
122                               140                               145                               150
124 CTG ATC CAA CTC TTC CAC AAA AAA ATT GAG TCT GCG CTT CGA AAC AAG      630
125 Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys
126                               155                               160                               165
128 ATG AAC AGC CAG GTC TGC GAG AAA GTG ACC AAT TCT GTA TCC TCC AAG      678

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129	Met	Asn	Ser	Gln	Val	Cys	Glu	Lys	Val	Thr	Asn	Ser	Val	Ser	Ser	Lys	
130	170					175					180					185	
132	CTG	CAA	CCT	TAT	TTC	CAG	ACT	CTG	CCA	GTA	ATG	ACC	AAA	ATA	GAT	TCT	726
133	Leu	Gln	Pro	Tyr	Phe	Gln	Thr	Leu	Pro	Val	Met	Thr	Lys	Ile	Asp	Ser	
134					190					195					200		
136	GTG	GCT	GGA	ATC	AAC	TAT	GGT	CTG	GTG	GCA	CCT	CCA	GCA	ACC	ACG	GCT	774
137	Val	Ala	Gly	Ile	Asn	Tyr	Gly	Leu	Val	Ala	Pro	Pro	Ala	Thr	Thr	Ala	
138				205					210					215			
140	GAG	ACC	CTG	GAT	GTA	CAG	ATG	AAG	GGG	GAG	TTT	TAC	AGT	GAG	AAC	CAC	822
141	Glu	Thr	Leu	Asp	Val	Gln	Met	Lys	Gly	Glu	Phe	Tyr	Ser	Glu	Asn	His	
142			220					225					230				
144	CAC	AAT	CCA	CCT	CCC	TTT	GCT	CCA	CCA	GTG	ATG	GAG	TTT	CCC	GCT	GCC	870
145	His	Asn	Pro	Pro	Pro	Phe	Ala	Pro	Pro	Val	Met	Glu	Phe	Pro	Ala	Ala	
146		235					240					245					
148	CAT	GAC	CGC	ATG	GTA	TAC	CTG	GGC	CTC	TCA	GAC	TAC	TTC	TTC	AAC	ACA	918
149	His	Asp	Arg	Met	Val	Tyr	Leu	Gly	Leu	Ser	Asp	Tyr	Phe	Phe	Asn	Thr	
150	250					255					260					265	
152	GCC	GGG	CTT	GTA	TAC	CAA	GAG	GCT	GGG	GTC	TTG	AAG	ATG	ACC	CTT	AGA	966
153	Ala	Gly	Leu	Val	Tyr	Gln	Glu	Ala	Gly	Val	Leu	Lys	Met	Thr	Leu	Arg	
154				270					275						280		
156	GAT	GAC	ATG	ATT	CCA	AAG	GAG	TCC	AAA	TTT	CGA	CTG	ACA	ACC	AAG	TTC	1014
157	Asp	Asp	Met	Ile	Pro	Lys	Glu	Ser	Lys	Phe	Arg	Leu	Thr	Thr	Lys	Phe	
158			285						290					295			
160	TTT	GGA	ACC	TTC	CTA	CCT	GAG	GTG	GCC	AAG	AAG	TTT	CCC	AAC	ATG	AAG	1062
161	Phe	Gly	Thr	Phe	Leu	Pro	Glu	Val	Ala	Lys	Lys	Phe	Pro	Asn	Met	Lys	
162			300					305					310				
164	ATA	CAG	ATC	CAT	GTC	TCA	GCC	TCC	ACC	CCG	CCA	CAC	CTG	TCT	GTG	CAG	1110
165	Ile	Gln	Ile	His	Val	Ser	Ala	Ser	Thr	Pro	Pro	His	Leu	Ser	Val	Gln	
166		315					320					325					
168	CCC	ACC	GGC	CTT	ACC	TTC	TAC	CCT	GCC	GTG	GAT	GTC	CAG	GCC	TTT	GCC	1158
169	Pro	Thr	Gly	Leu	Thr	Phe	Tyr	Pro	Ala	Val	Asp	Val	Gln	Ala	Phe	Ala	
170	330					335					340					345	
172	GTC	CTC	CCC	AAC	TCC	CTG	GCT	TCC	CTC	TTC	CTG	ATT	GGC	ATG	CAC		1206
173	Val	Leu	Pro	Asn	Ser	Ser	Leu	Ala	Ser	Leu	Phe	Leu	Ile	Gly	Met	His	
174				350					355						360		
176	ACA	ACT	GGT	TCC	ATG	GAG	GTC	AGC	GCC	GAG	TCC	AAC	AGG	CTT	GTT	GGA	1254
177	Thr	Thr	Gly	Ser	Met	Glu	Val	Ser	Ala	Glu	Ser	Asn	Arg	Leu	Val	Gly	
178			365						370					375			
180	GAG	CTC	AAG	CTG	GAT	AGG	CTG	CTC	CTG	GAA	CTG	AAG	CAC	TCA	AAT	ATT	1302
181	Glu	Leu	Lys	Leu	Asp	Arg	Leu	Leu	Leu	Glu	Leu	Lys	His	Ser	Asn	Ile	
182			380					385					390				
184	GGC	CCC	TTC	CCG	GTT	GAA	TTG	CTG	CAG	GAT	ATC	ATG	AAC	TAC	ATT	GTA	1350
185	Gly	Pro	Phe	Pro	Val	Glu	Leu	Leu	Gln	Asp	Ile	Met	Asn	Tyr	Ile	Val	
186		395				400						405					
188	CCC	ATT	CTT	GTG	CTG	CCC	AGG	GTT	AAC	GAG	AAA	CTA	CAG	AAA	GGC	TTC	1398
189	Pro	Ile	Leu	Val	Leu	Pro	Arg	Val	Asn	Glu	Lys	Leu	Gln	Lys	Gly	Phe	
190	410					415					420					425	
192	CCT	CTC	CCG	ACG	CCG	GCC	AGA	GTC	CAG	CTC	TAC	AAC	GTA	GTG	CTT	CAG	1446
193	Pro	Leu	Pro	Thr	Pro	Ala	Arg	Val	Gln	Leu	Tyr	Asn	Val	Val	Leu	Gln	

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194          430          435          440
196 CCT CAC CAG AAC TTC CTG CTG TTC GGT GCA GAC GTT GTC TAT AAA      1491
197 Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys
198          445          450          455
200 TGAAGGCACC AGGGGTGCCG GGGGCTGTCA GCCGCACCTG TTCCTGATGG GCTGTGGGGC      1551
202 ACCGGCTGCC TTTCCCCAGG GAATCCTCTC CAGATCTTAA CCAAGAGCCC CTTGCAAACT      1611
204 TCTTCGACTC AGATTCAGAA ATGATCTAAA CACGAGGAAA CATTATTCAT TGGAAAAGTG      1671
206 CATGGTGTGT ATTTTAGGGA TTATGAGCTT CTTTCAAGGG CTAAGGCTGC AGAGATATTT      1731
208 CCTCCAGGAA TCGTGTTCAT ATTGTAACCA AGAAATTTCC ATTTGTGCTT CATGAAAAAA      1791
210 AACTTCTGGT TTTTTCATG TG      1813
213 (2) INFORMATION FOR SEQ ID NO: 2:
215     (i) SEQUENCE CHARACTERISTICS:
216         (A) LENGTH: 487 amino acids
217         (B) TYPE: amino acid
218         (D) TOPOLOGY: linear
220     (ii) MOLECULE TYPE: protein
222     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
224 Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val
225 -31 -30          -25          -20
227 Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
228 -15          -10          -5          1
230 Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
231          5          10          15
233 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
234          20          25          30
236 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
237          35          40          45
239 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
240 50          55          60          65
242 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
243          70          75          80
245 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
246          85          90          95
248 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
249          100          105          110
251 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
252          115          120          125
254 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
255 130          135          140          145
257 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
258          150          155          160
260 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
261          165          170          175
263 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
264          180          185          190
266 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
267          195          200          205
269 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
270 210          215          220          225

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```

272 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
273          230          235          240
275 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
276          245          250          255
278 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
279          260          265          270
281 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
282          275          280          285
284 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
285 290          295          300          305
287 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
288          310          315          320
290 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
291          325          330          335
293 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
294          340          345          350
296 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
297          355          360          365
299 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
300 370          375          380          385
302 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
303          390          395          400
305 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
306          405          410          415
308 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
309          420          425          430
311 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
312          435          440          445
314 Gly Ala Asp Val Val Tyr Lys
315 450          455

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/696,709

DATE: 11/10/2004

TIME: 10:22:28

Input Set : N:\Crf3\RULE60\09696709.raw.txt

Output Set: N:\CRF4\11102004\I696709.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:34 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)  
L:36 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)